AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. (Currently amended): A method of data analysis for determining a base sequence for nucleic acid, based on detected data of electrophoresis of a fragment sample of nucleic acid, comprising steps of:

(A) performing waveform shaping by Fourier transformation on data of a certain number N of points from the head of the detected data ~~with a parameter of a previously set~~ using a predetermined peak interval as a parameter;

(B) determining the base sequence as to data of P points (P < N) from the head of the data of N points;

(C) obtaining a subsequent peak interval from the result of the most recent sequence determination;

(D) performing waveform shaping by Fourier transformation on data of N points starting from a position returning by L points (L < M) from ~~final data precedently~~ a final point of the data most recently subjected to the sequence determination ~~with a parameter of a precedently obtained~~ using the subsequent peak interval as a parameter; and

(E) determining the base sequence as to data of M points (M < N) of a central portion among the data of N points subjected to ~~second or later~~ waveform shaping in step (D), so as to be connected with data ~~precedently~~ most recently subjected to the sequence determination, wherein

the steps (E) → (C) → (D) are repeated until ~~data disappear~~ all data has been analyzed or no analysis is required despite presence of data.

2. (Currently amended): The method of data analysis for determining a base sequence for nucleic acid according to claim 1, wherein

FFT treatment is applied to at least one of steps (A) or (D) as the waveform shaping by Fourier transformation.

3. (Currently amended): The method of data analysis for determining a base sequence for nucleic acid according to claim 2, assuming that N is equal to 2^n, M is equal to $2^{(n-1)}$ and L is equal to $2^{(n-2)}$.